CLAIM LISTING

Claim 1 (Currently Amended): A method of monitoring a gene expression profile ~~identifying a gene~~ associated with oral cancer comprising:

contacting a first array of probes with a first population of nucleic acids derived from a human subject from one or more cells obtained from malignant oral tissue;

contacting a second array of probes with a second population of nucleic acids derived from the human subject from one or more cells obtained from normal oral tissue; and

determining relative hybridization of the first array of probes to the first population of nucleic acids relative to hybridization of the second array of probes to the second population of nucleic acids, wherein [[a]] nucleic acids [[gene]] that ~~hybridizes~~ hybridize differently correspond to genes of a gene expression profile that are [[is]] associated with oral cancer, and wherein the genes of a gene expression profile are selected from the group consisting of p-53 responsive gene 2, beta A inhibin, human alpha-1 collagen type I gene, placental protein 11, BENE protein, neuromedin U, flavin containing monooxygenase 2, runt-related transcription factor 1, alpha 2 collagen type I, fibrillin 1, lysophospholipase-like, absent in melanoma 1, nonvoltage-gated 1 alpha sodium channel, protein tyrosine kinase 6 and epithelial membrane protein 1.

Claim 2 (Currently Amended): A method of expression monitoring comprising:

contacting a first array of probes with a first population of nucleic acids derived from at least one cell derived from normal tissue from a human subject;

contacting a second array of probes with a second population of nucleic acids derived from at least one cell derived from malignant oral tissue from the human subject; and

determining binding of the first array of probes to the nucleic acids from the first population relative to [[the]] binding of the second array of probes to the nucleic acids from the second population to identify at least one probe binding to a nucleic acid [[gene]] that is differentially expressed between the first and second populations, wherein the nucleic acid corresponds to a gene selected from the group consisting of p-53 responsive gene 2, beta A inhibin, human alpha-1 collagen type I gene, placental protein 11, BENE protein, neuromedin U, flavin containing monooxygenase 2, runt-related transcription factor 1, alpha 2 collagen type I,

fibrillin 1, lysophospholipase-like, absent in melanoma 1, nonvoltage-gated 1 alpha sodium channel, protein tyrosine kinase 6 and epithelial membrane protein 1.

Claims 3-6 (Cancelled)

Claim 7 (Currently Amended): A method of diagnosing a human subject with oral cancer, the method comprising:

detecting [[the]] a level of expression of a marker selected from a group of markers associated with oral cancer in a test sample from the human subject; and

detecting the level of expression of the marker in a control sample from normal tissue from the human subject,

wherein the level of expression of the marker in the control sample differs from the level of expression of the marker in the test sample when the subject is afflicted with oral cancer, and wherein the group of markers associated with oral cancer corresponds to a group of genes comprising p-53 responsive gene 2, beta A inhibin, human alpha-1 collagen type I gene, placental protein 11, BENE protein, neuromedin U, flavin containing monooxygenase 2, runt-related transcription factor 1, alpha 2 collagen type I, fibrillin 1, lysophospholipase-like, absent in melanoma 1, nonvoltage-gated 1 alpha sodium channel, protein tyrosine kinase 6 or epithelial membrane protein 1.

Claim 8 (Currently Amended): The method of claim 7, wherein the test sample from the subject comprises cells obtained from the subject.

Claim 9 (Original): The method of claim 8, wherein the cells are obtained from oral tissue.

Claim 10 (Original): The method of claim 8, wherein the cells are obtained from blood cells.

Claim 11 (Previously Presented): The method of claim 7, wherein the levels of expression of the marker in the control sample and in the test sample are assessed by a method comprising:

contacting a first array of probes with a first population of nucleic acids derived from one or more cells from the test sample;

contacting a second array of probes with a second population of nucleic acids derived from one or more cells from the control sample; and

determining relative hybridization of the first array of probes to the first population of nucleic acids to relative hybridization of the second array of probes to the second population of nucleic acids.

Claim 12 (Previously Presented): The method of claim 11, wherein the first and second population of nucleic acids are RNA.

Claim 13 (Previously Presented): The method of claim 11, wherein the first and second population of nucleic acids are DNA.

Claim 14 (Previously Presented): The method of claim 11, wherein the first population of nucleic acids is amplified prior to contacting to the first array of probes or the second population of nucleic acids is amplified prior to contacting the second array of probes.

Claims 15-17 (Cancelled)

Claim 18 (Previously Presented): The method of claim 7, wherein the marker is a nucleic acid.

Claim 19 (Original): The method of claim 18, wherein the nucleic acid is RNA.

Claim 20 (Original): The method of claim 18, wherein the nucleic acid is DNA.

Claim 21 (Original): The method of claim 18, wherein one or more nucleic acids is amplified prior to assessing the sample.

Claim 22 (Currently Amended): A method for monitoring the progression of oral cancer in a human subject, the method comprising:

detecting in a first sample obtained from the human subject at a first point in time, a level of expression of a marker selected from a group of markers associated with oral cancer;

detecting in a subsequent sample obtained from the human subject at a subsequent point in time, the level of expression of the marker, and

comparing the level of expression detected in the first and subsequent detecting samples in order to monitor the progression of oral cancer, wherein the group of markers associated with oral cancer corresponds to a group of genes comprising p-53 responsive gene 2, beta A inhibin, human alpha-1 collagen type I gene, placental protein 11, BENE protein, neuromedin U, flavin containing monooxygenase 2, runt-related transcription factor 1, alpha 2 collagen type I, fibrillin 1, lysophospholipase-like, absent in melanoma 1, nonvoltage-gated 1 alpha sodium channel, protein tyrosine kinase 6 or epithelial membrane protein 1.

Claim 23 (Previously Presented): The method of claim 22, wherein the first and the subsequent samples comprise cells obtained from the subject.

Claim 24 (Original): The method of claim 23, wherein the cells are obtained from oral tissue.

Claim 25 (Original): The method of claim 23, wherein the cells obtained are blood cells.

Claims 26-36 (Cancelled)

Claim 37 (New): The method of claim 7, wherein the control sample from the subject comprises cells obtained from the subject.